

47006

Schreiber, David

From: Fronda, Christian
Sent: Tuesday, July 17, 2001 5:32 PM
To: Schreiber, David
Subject: Protein Sequence Search on Serial No. 09/435,770
Importance: High.

Hi David, can you perform a protein sequence search on Serial No. 09/435,770 which is listed below. Thank you very much.

Christian L. Fronda
Art Unit 1652
(703)305-1252

Please perform sequence search and interference search for Serial No. 09/435,770

1. Please search SEQ ID Nos.: 1-6 against amino acid databases including pending and issued.

Please save on COMPUTER DISKETTES.

Please save results from interference searches on different diskettes from the commercial and issued search results.

Thank you very much.

Sincerely,
Chris Fronda
CM1 10B13
AU 1652
305-1252

RAW SEQUENCE LISTING

DATE: 07/17/2001

PATENT APPLICATION: US/09/435,770B

TIME: 17:20:10

Input Set : N:\CrF3\07132001\I435770B.raw

Output Set: N:\CRF3\07172001\I435770B.raw

1 <110> APPLICANT: YAMAMOTO, Takuo
 2 MARUTA, Kazuhiko
 3 KUBOTA, Michio
 4 FUKUDA, Shigeharu
 5 MIYAKE, Toshio
 6 <120> TITLE OF INVENTION: NON-REDUCING SACCHARIDE-FORMING ENZYME,
 7 TREHALOSE-RELEASING ENZYME, AND PROCESS FOR PRODUCING
 8 SACCHARIDES USING THE ENZYMES
 9 <130> FILE REFERENCE: YAMAMOTO=16A
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/435,770B
 11 <141> CURRENT FILING DATE: 1999-11-08
 12 <150> PRIOR APPLICATION NUMBER: JP 258,394/1998
 13 <151> PRIOR FILING DATE: 1998-09-11
 14 <150> PRIOR APPLICATION NUMBER: JP 352,252/1998
 15 <151> PRIOR FILING DATE: 1998-12-11
 16 <150> PRIOR APPLICATION NUMBER: JP 16,931/1999
 17 <151> PRIOR FILING DATE: 1999-01-26
 18 <160> NUMBER OF SEQ ID NOS: 39
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 756
 23 <212> TYPE: PRT
 24 <213> ORGANISM: ARTHROBACTER sp.S34
 25 <400> SEQUENCE: 1
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 27 1 5 10 15
 28 Asp Ala Ala Arg Ile Val Pro Tyr Leu His Arg Leu Gly Ala Asp Trp
 29 20 25 30
 30 Leu Tyr Leu Ser Pro Leu Leu Glu Ser Glu Ser Gly Ser Ser His Gly
 31 35 40 45
 32 Tyr Asp Val Val Asp His Ser Arg Val Asp Ala Ala Arg Gly Gly Pro
 33 50 55 60
 34 Glu Gly Leu Ala Glu Leu Ser Arg Ala Ala His Glu Arg Gly Met Gly
 35 65 70 75 80
 36 Val Val Val Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Lys
 37 85 90 95
 38 Ala Asn Arg Trp Trp Trp Asp Val Leu Ala Arg Gly Gln Arg Ser Glu
 39 100 105 110
 40 Tyr Ala Asp Tyr Phe Asp Ile Asp Trp Glu Phe Gly Gly Gly Arg Leu
 41 115 120 125
 42 Arg Leu Pro Val Leu Gly Asp Gly Pro Asp Glu Leu Asp Ala Leu Arg
 43 130 135 140
 44 Val Asp Gly Asp Glu Leu Val Tyr Tyr Glu His Arg Phe Pro Ile Ala
 45 145 150 155 160
 46 Glu Gly Thr Gly Gly Gly Thr Pro Arg Glu Val His Asp Arg Gln His
 47 165 170 175
 48 Tyr Glu Leu Met Ser Trp Arg Arg Ala Asp His Asp Leu Asn Tyr Arg

ENTERED
P.5

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49          180          185          190
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52  Arg Val Phe Asp Asp Thr His Arg Glu Ile Gly Arg Trp Ile Ala Glu
53          210          215          220
54  Gly Leu Val Asp Gly Leu Arg Val Asp His Pro Asp Gly Leu Arg Ala
55          225          230          235          240
56  Pro Gly Asp Tyr Leu Arg Arg Leu Ala Glu Leu Ala Gln Gly Arg Pro
57          245          250          255
58  Ile Trp Val Glu Lys Ile Ile Glu Gly Asp Glu Arg Met Pro Pro Gln
59          260          265          270
60  Trp Pro Ile Ala Gly Thr Thr Gly Tyr Asp Ala Leu Ala Gly Ile Asp
61          275          280          285
62  Arg Val Leu Val Asp Pro Ala Gly Glu His Pro Leu Thr Gln Ile Val
63          290          295          300
64  Asp Glu Ala Ala Gly Ser Pro Arg Arg Trp Ala Glu Leu Val Pro Glu
65          305          310          315          320
66  Arg Lys Arg Ala Val Ala Arg Gly Ile Leu Asn Ser Glu Ile Arg Arg
67          325          330          335
68  Val Ala Arg Glu Leu Gly Glu Val Ala Gly Asp Val Glu Asp Ala Leu
69          340          345          350
70  Val Glu Ile Ala Ala Ala Leu Ser Val Tyr Arg Ser Tyr Leu Pro Phe
71          355          360          365
72  Gly Arg Glu His Leu Asp Glu Ala Val Ala Ala Ala Gln Ala Ala Ala
73          370          375          380
74  Pro Gln Leu Glu Ala Asp Leu Ala Ala Val Gly Ala Ala Leu Ala Asp
75          385          390          395          400
76  Pro Gly Asn Pro Ala Ala Leu Arg Phe Gln Gln Thr Ser Gly Met Ile
77          405          410          415
78  Met Ala Lys Gly Val Glu Asp Asn Ala Phe Tyr Arg Tyr Pro Arg Leu
79          420          425          430
80  Thr Ser Leu Thr Glu Val Gly Gly Asp Pro Ser Leu Phe Ala Ile Asp
81          435          440          445
82  Ala Ala Ala Phe His Ala Ala Gln Arg Asp Arg Ala Ala Arg Leu Pro
83          450          455          460
84  Glu Ser Met Thr Thr Leu Thr Thr His Asp Thr Lys Arg Ser Glu Asp
85          465          470          475          480
86  Thr Arg Ala Arg Ile Thr Ala Leu Ala Glu Ala Pro Glu Arg Trp Arg
87          485          490          495
88  Arg Phe Leu Thr Glu Val Gly Gly Leu Ile Gly Thr Gly Asp Arg Val
89          500          505          510
90  Leu Glu Asn Leu Ile Trp Gln Ala Ile Val Gly Ala Trp Pro Ala Ser
91          515          520          525
92  Arg Glu Arg Leu Glu Ala Tyr Ala Leu Lys Ala Ala Arg Glu Ala Gly
93          530          535          540
94  Glu Ser Thr Asp Trp Ile Asp Gly Asp Pro Ala Phe Glu Glu Arg Leu
95          545          550          555          560
96  Thr Arg Leu Val Thr Val Ala Val Glu Glu Pro Leu Val His Glu Leu
97          565          570          575

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98      Leu Glu Arg Leu Val Asp Glu Leu Thr Ala Ala Gly Tyr Ser Asn Gly
99              580              585              590
100     Leu Ala Ala Lys Leu Leu Gln Leu Leu Ala Pro Gly Thr Pro Asp Val
101              595              600              605
102     Tyr Gln Gly Thr Glu Arg Trp Asp Arg Ser Leu Val Asp Pro Asp Asn
103              610              615              620
104     Arg Arg Pro Val Asp Phe Ala Ala Ala Ser Glu Leu Leu Asp Arg Leu
105              625              630              635              640
106     Asp Gly Gly Trp Arg Pro Pro Val Asp Glu Thr Gly Ala Val Lys Thr
107              645              650              655
108     Leu Val Val Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu Leu
109              660              665              670
110     Phe Thr Ala Tyr His Pro Val Thr Ala Arg Gly Ala Gln Ala Glu His
111              675              680              685
112     Leu Ile Gly Phe Asp Arg Gly Gly Ala Ile Ala Leu Ala Thr Arg Leu
113              690              695              700
114     Pro Leu Gly Leu Ala Ala Ala Gly Gly Trp Gly Asp Thr Val Val Asp
115              705              710              715              720
116     Val Gly Glu Arg Ser Leu Arg Asp Glu Leu Thr Gly Arg Glu Ala Arg
117              725              730              735
118     Gly Ala Ala Arg Val Ala Glu Leu Phe Ala Asp Tyr Pro Val Ala Leu
119              740              745              750
120     Leu Val Glu Thr
121              755
123 <210> SEQ ID NO: 2
124 <211> LENGTH: 6
125 <212> TYPE: PRT
126 <213> ORGANISM: ARTHROBACTER sp.S34
127 <400> SEQUENCE: 2
128     Asp Ile Val Pro Asn His
129         1              5
131 <210> SEQ ID NO: 3
132 <211> LENGTH: 6
133 <212> TYPE: PRT
134 <213> ORGANISM: ARTHROBACTER sp.S34
135 <400> SEQUENCE: 3
136     Gly Thr Thr Gly Tyr Asp
137         1              5
139 <210> SEQ ID NO: 4
140 <211> LENGTH: 20
141 <212> TYPE: PRT
142 <213> ORGANISM: ARTHROBACTER sp.S34
143 <400> SEQUENCE: 4
144     Pro Ala Ser Thr Tyr Arg Leu Gln Ile Ser Ala Glu Phe Thr Leu Phe
145         1              5              10              15
146     Asp Ala Ala Arg
147              20
149 <210> SEQ ID NO: 5
150 <211> LENGTH: 20

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Input Set : N:\Cr3\07132001\I435770B.raw

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151 <212> TYPE: PRT
152 <213> ORGANISM: ARTHROBACTER sp.S34
153 <400> SEQUENCE: 5
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155         1             5             10             15
156     Ser Glu Leu Leu
157         20
159 <210> SEQ ID NO: 6
160 <211> LENGTH: 20
161 <212> TYPE: PRT
162 <213> ORGANISM: ARTHROBACTER sp.S34
163 <400> SEQUENCE: 6
164     Ala Asn Arg Trp Trp Trp Asp Val Leu Ala Arg Gly Gln Arg Ser Glu
165         1             5             10             15
166     Tyr Ala Asp Tyr
167         20
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170 <211> LENGTH: 2268
171 <212> TYPE: DNA
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174     cccgccagta cctaccgcct tcagatctcg gcggagttca ccctcttcga cgcggcgcg 60
175     atcgtgccct acctgcaccg cctcgcgccc gactggctgt acctctcgcc gctgctcgag 120
176     tccgagtcgg gctcctcgca cggctacgac gtggtcgacc actcccgctg cgacgccgcc 180
177     cgcggcgggc cggaggggct cgccgagctc tcccgctcgg cgcacgagcg cgccatgggc 240
178     gtcgtcgtcg acatcgtgcc caaccacgtc ggctcgcca cgccgaaggc gaaccgctgg 300
179     tggtagggac ttctggcccg tggacagcgg tcggagtacg ccgactactt cgacatcgac 360
180     tgggagttcg gcggcgccag gctgcgcctg cccgtgctcg gcgacggccc cgacgagctc 420
181     gacgcgctga gactggatgg cgacgagctc gtctactacg agcaccgctt cccgatcgcc 480
182     gagggcaccg gcggcgccac cccgcgcgag gtgcacgacc ggcagcacta cgagctgatg 540
183     tcgtggcggc gggccgacca cgacctcaac taccgcccgt tcttcgccgt gaacacgctc 600
184     gccgccgtac gcgtcgaaga cccgcgcgtg ttcgacgaca cccaccgcca gatcggccgc 660
185     tggatcgccg agggcctcgt cgacggcctg cgctcgacc accccgacgg gctgcgcgcc 720
186     cccggcgact acctgcgccg tctcgccgag ctgcgccaaag gcaggccgat ctgggtcgag 780
187     aagatcatcg agggcgacga gcggatgccc ccgagtgggc ccacgcccgg caccaccggc 840
188     tacgacgcgc tggccgggat cgaccgggtg ctgctcgacc ccgcgggcca gcatccgctc 900
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191     ctcgagagag tcgcccgcga cgtcgaagac gcgctcgtcg agatcgccgc cgccctgtcc 1080
192     gtctaccgca gctacctgcc gttcgggccc gagcacctcg acgaagccgt ggccgcccgc 1140
193     caggccgagc ccccccagct cgaggccgac ctgcgcgccc tcggcgagc gctcgccgac 1200
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196     gaccgagacc tgctcgcat cgacgcggcc gccttccacg cggcgagcgc cgaccgcgcc 1380
197     gcccggctgc ccgagtcgat gacgacgctg accaccacag acaccaagcg cagcgaagac 1440
198     acccgggccc ggatcacgcg gctcgccgag gccccgaac gctggcgggc cttcctgacc 1500
199     gaggtcggcg ggctcatcgg aacgggcgac cgggtgctgg agaacctgat ctggcaggcg 1560
200     atcgtcggcg cgtggccggc gagccgggag cggctcgagg cctacgcgct gaaggccgcg 1620
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Input Set : N:\Cr3\07132001\I435770B.raw

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204      ctgcccccg gaacccccga cgtgtaccag ggcacggaac gctgggaccg gtcgctgggtg 1860
205      gaccgggaca accgtcgccc cgtggatttc gccgcggcat ccgagctgct cgaccgcctc 1920
206      gacggcggct ggcgggccgc cgtcgacgag accggcgcggt tcaagacgct cgtcgtctcc 1980
207      cgcgcgctgc ggctgcggcg cgaccggccc gagctgttca ccgctacca cccggtcacg 2040
208      gcgcgcggcg cgcaggccga gcacctgac ggcttcgacc gcggcggcgc gatcgccctg 2100
209      gccaccgcc tgccgctcgg cctcgccgcc gcaggcggtt ggggcgacac ggtcgtcgac 2160
210      gtcggcgagc ggagcctgcg cgacgagctg accggccgcg agggccgcgg agcggcgcg 2220
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213 <210> SEQ ID NO: 8
214 <211> LENGTH: 28
215 <212> TYPE: DNA
216 <213> ORGANISM: ARTHROBACTER sp.S34
217 <400> SEQUENCE: 8
218      tttttaata aaatcaggag gaaaaaat 28
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221 <211> LENGTH: 575
222 <212> TYPE: PRT
223 <213> ORGANISM: ARTHROBACTER sp.S34
224 <400> SEQUENCE: 9
225      Met Asn Arg Arg Phe Pro Val Trp Ala Pro Gln Ala Ala Gln Val Thr
226      1 5 10 15
227      Leu Val Val Gly Gln Gly Arg Ala Glu Leu Pro Leu Thr Arg Asp Glu
228      20 25 30
229      Asn Gly Trp Trp Ala Leu Gln Gln Pro Trp Asp Gly Gly Pro Asp Leu
230      35 40 45
231      Val Asp Tyr Gly Tyr Leu Val Asp Gly Lys Gly Pro Phe Ala Asp Pro
232      50 55 60
233      Arg Ser Leu Arg Gln Pro Arg Gly Val His Glu Leu Gly Arg Glu Phe
234      65 70 75 80
235      Asp Pro Ala Arg Tyr Ala Trp Gly Asp Asp Gly Trp Arg Gly Arg Asp
236      85 90 95
237      Leu Thr Gly Ala Val Ile Tyr Glu Leu His Val Gly Thr Phe Thr Pro
238      100 105 110
239      Glu Gly Thr Leu Asp Ser Ala Ile Arg Arg Leu Asp His Leu Val Arg
240      115 120 125
241      Leu Gly Val Asp Ala Val Glu Leu Leu Pro Val Asn Ala Phe Asn Gly
242      130 135 140
243      Thr His Gly Trp Gly Tyr Asp Gly Val Leu Trp Tyr Ala Val His Glu
244      145 150 155 160
245      Pro Tyr Gly Gly Pro Glu Ala Tyr Gln Arg Phe Val Asp Ala Cys His
246      165 170 175
247      Ala Arg Gly Leu Ala Val Val Gln Asp Val Val Tyr Asn His Leu Gly
248      180 185 190
249      Pro Ser Gly Asn His Leu Pro Asp Phe Gly Pro Tyr Leu Gly Ser Gly
250      195 200 205
251      Ala Ala Asn Thr Trp Gly Asp Ala Leu Asn Leu Asp Gly Pro Leu Ser
252      210 215 220

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

fil

7/17/01

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/435,770B

DATE: 07/17/2001

TIME: 17:20:11

Input Set : N:\Crf3\07132001\I435770B.raw

Output Set: N:\CRF3\07172001\I435770B.raw

L:10 M:270 C: Current Application Number differs, Wrong Format

L:681 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31

L:684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31